

Figure 1

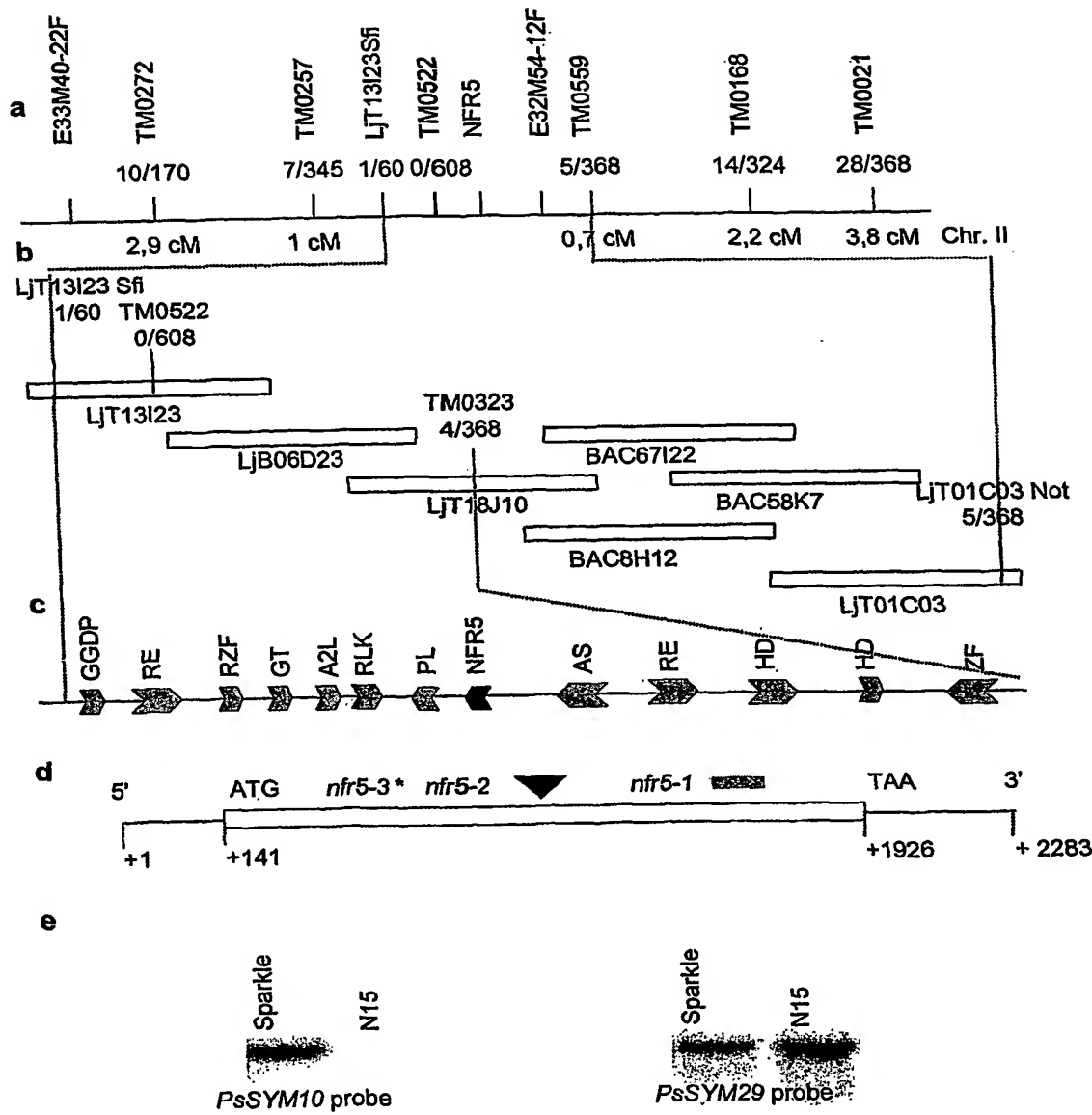
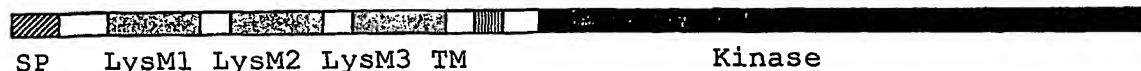


Figure 2**a**

SP LysM1 LysM2 LysM3 TM Kinase

b

MAVFFLTSGSLSLFLALTLLFTNIAA SP

RSEKISGPDFSCPVDSPSPSCETYVT 51 aa

*
YTAQSPNLLSLTNISDIFDISPLSIARASNIDAGKDKLVPGQVLLVP LysM1

VTCCGAGNHSSANTS 113 aa

YQIQLGDSYDFVATTLYENLTNWNIVQASNPGVNPYLLPERVKVVFP LysM2

LFRCRPSKNQLNKGIQYLIT 180 aa

YVWKPNDNVSLVSAKFGASPADILTENRYGQDFTAATNLPILIP LysM3

VTQLPELTQPSSNGRKSSIHL 246 aa

VILGITLGCTLLTAVLTGTLVYVYC TM

RRKKALNRTASSAETADKLLSGVSGYVSKPNVYEIDEI KD

I
MEATKDFSDECKVGESVYKANIEGRVVAVKKIKEGGANEELKILQKV

II III
NHGNLVKLMGVSSGYDGNCFLVYEYAENGSLAEWLFSKSSGTPNSLT

IV V
WSQRISIAVDVAVGLQYMHEHTYPRIIHRDITTSNILLDSNFKAKIA

VIa Vlb
NFAMARTSTNPMMPKIDVFAFGVLLIELLTGRKAMTTKENGEEVVMLW

VII IX
KDMWEIFDIEENREERIRKWMDPNLESFYHIDNALSASLAVNCTAD

KSLSRPSMAEIVLSLSFLTQQSSNPTLERSLTSSGLDVEDDAHIVTS

XI
ITAR 595 aa

Figure 2

c

NFR5M1 52: YTAOSP~~NTLS~~LTN~~ISD~~IFDIS~~PL~~SIARAS~~NED~~AGDK~~LV~~EGOV~~LL~~VP:98
 SYM10M1 52: YFARSP~~NFL~~SLTN~~ISD~~IFDMS~~PL~~SIAKAS~~NED~~EDDK~~LV~~EGOV~~LL~~IP:98
 M.tM1 53: YRAOSP~~NFL~~SLTN~~ISD~~IFENL~~SP~~TRIAKAS~~NED~~EDDK~~LV~~EDOL~~LL~~VP:99
 RiceM1 47: YRTQSPG~~FLD~~LGN~~ISD~~LEGVSRALIASANKLT~~TE~~GV~~LL~~EGO~~PL~~LV:93

NFR5M2 114: YQIQLED~~SYDF~~VAT~~TL~~EN~~ET~~INWNI~~QAS~~NPCV~~NBY~~LLHERV~~KV~~VP:160
 SYM10M2 114: YTEKLED~~NYE~~LVST~~TS~~YONET~~NY~~VEMENF~~NPN~~ESPN~~LL~~RPET~~KV~~VP:160
 M.tM2 115: YSTKQGD~~NRE~~LLSIT~~SY~~QNE~~TY~~LEFKNF~~NPN~~ESPT~~LL~~ELDT~~KV~~VP:161
 RiceM2 109: YPTRP~~PD~~TEGLAVIRAFEN~~ET~~DF~~LV~~EELN~~EAA~~EATRLEP~~WQ~~EV~~VP~~:155
 VolvoxM2 106: YLTQPG~~DE~~WAI~~AQR~~.RG..~~ET~~VDVIQ~~SIN~~PGV~~N~~EARLQV~~GO~~VIN~~VP~~:149
 Pfam 1: YTVKKG~~DTL~~WKIARR.~~YG~~..ISVSELKSLN.~~GL~~SSDNL~~YV~~GCKLKIP:43

NFR5M3 181: YVWKEND~~NVS~~LVSAK~~KE~~ASPA~~IL~~TENRYG~~OD~~FTAAT~~NL~~ILIP:224
 SYM10M3 181: YVWOAND~~NV~~TRVSS~~KE~~GASQ~~VDM~~FTE~~N~~..~~NON~~FTAST~~NV~~EILIP:222
 M.tM3 182: YVWOD~~ND~~NVTLVSS~~KE~~GASQ~~VEM~~TAEN..~~NH~~FTAST~~NR~~SVLIP:223
 RiceM3 176: YVWQPG~~DD~~SVVSALMN~~ASA~~ANIAASNGVAG~~NST~~FATGQ~~EV~~LIP:219

d

	VII	VIII	IX
Cons	... <u>DFG</u> <u>APG</u> <u>D.W</u> ..G
Smart 195:	K TA D E G L S F ..DLYSD E YYKVKGGKLP	IRWMA P ESLKEGKFTSKSDVWSFG:248	
Arab 500:	K TA N F Q V ARILDEG L DLQLTRHVEGTQGYLA	PEYVENGVITSKLDVRAFG:550	
NFR5 448:	K TA N F AMARIS N	PMMPK ED VDVRAFG:472	
SYM10 449:	K TA N F S AR TS EN	SMMPK ED VDVRAFG:473	
M.t 450:	K TA N F AMARIS N	SMMPK ED VDVRAFG:474	
Rice 476:	K L S N ESL K PAAMV D	AAATSSD V RAFG:502	

Figure 4

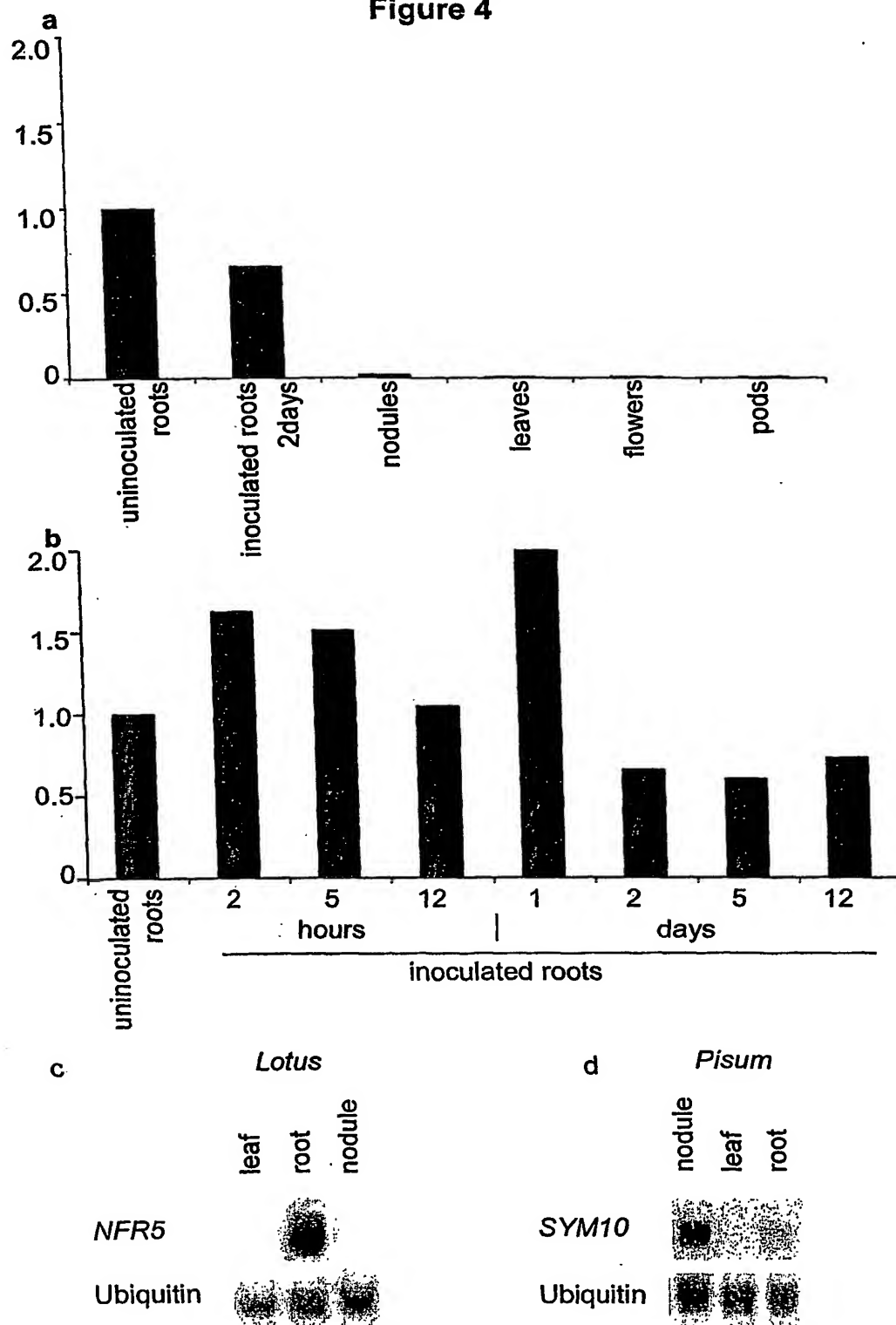


Figure 5

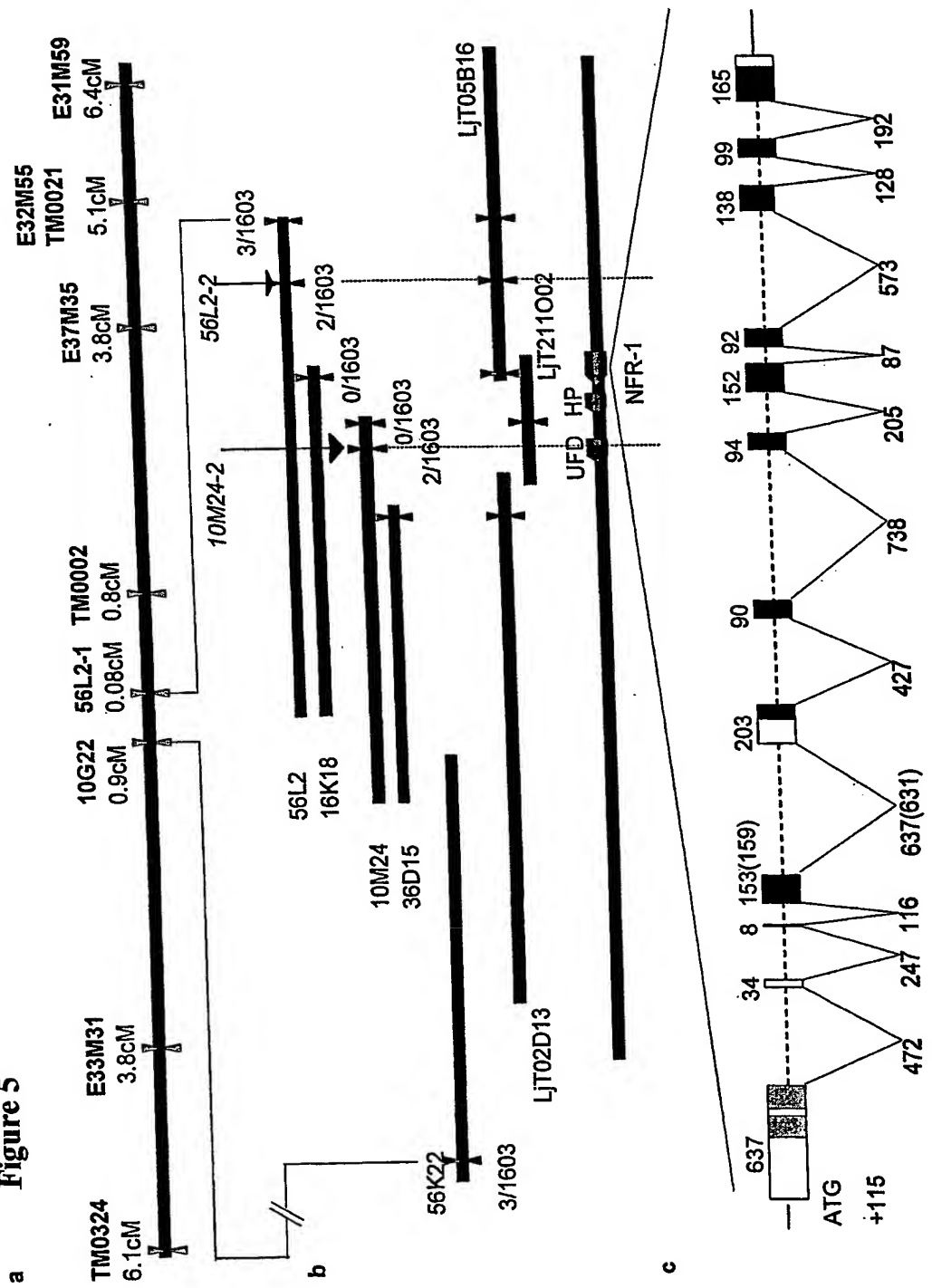


Figure 6

a

MKLKTGLLLFFILLGH SP
 VCFHVESNCLKGCDLALASYIILPGVFILQNITTFMQSEIVSSNDAITS
 YNKDKIILNDINIQSFORLNIPFPCDCIGGEFLGHVFE 103
YSASKGDTYETIANLYANLTTVDLLKRENSYPKNIPVNAKVNVT LysM1
 VNCSCGNSQVSKDYGLFIT 168
YPIRPGDTLQDIANQSSLDAGLIQSFNPSVNFSKDSGIAFIP LysM2
 GRYKNGVYVPLYHR 224
 TAGLASGAAVGISIAGTFVLLLLAFCMYV TM
 RYQKKEEEKAKLPDDISMALSTQD(GN)A,SSSAEYETSGSSGPGTASAT
 GLTSIMVAKSMEFSYQELAKATNN 322 (324)
 FSLDNKIGOGGFGAVYYAELRGKKTAIKKMDVQASTEFFLCELKVLTHV KD
 I II III
 HHLNLVRLIGYCVESLFLVYEHIDNGNLGQYLHGSGKEPLPWSSRVOIA
 IV V VIa
 LDAARGLEYIHEHTVPVYIHRDVKSANILIDKNLRGKVADFGLTKLIEVG
 VIa Vib VII
 NSTLQTRLVGTFGYMPPEYAQYGDISPKIDVYAFGVVLFELISAKNAVLKT 621 (623)
 VIII * IX
 GELVAESKGLVALFEEALNKSDPCDALRKLVDPRLGENYPIDSVLKIAQLG
 *
 RACTRDNPLLRPSMRSLVVALMTLSSLTEDCDESSYESQTLINLLSVR*
 XI

b

SMART0257 YTVKKCDTLSS IARRYGISVS --DTELMNILD EDNLQVGO KIP-
 NFR1-M1 104 YSAS GDTYET IANLYAN LTVD LLKRE NSYD EKN EAN V N T --149
 At21630-M1 105 YSVRQED T RVA ISNY ANLT MES LQAR NPF PAT N LS T E N LV -151
 SMART0257 YTVKKCDTLSS IARRYGISVS VSD LLE NN -ILD DNLQV QKL KIP
 NFR1-M2 167 YPIR P GDT LQDI ANQ SSLD AGLI QS F N S V A D I R Y N S G N G --VY V P -211
 At21630-M2 170 VPLR E D S S S I A R S S G V A D I R Y N S G N G --VY V P -211
 BAB89226-M2 168 YAVQ D C D I G N I A S L F R S W K D I L D E N R V A N D F I K P E W L F I P -212
 Volvox M 42 YTIQ R G D F W A I Q R F T T V D V I Q S E N S G N P A R L Q V Q V I N V P -85

Figure 7

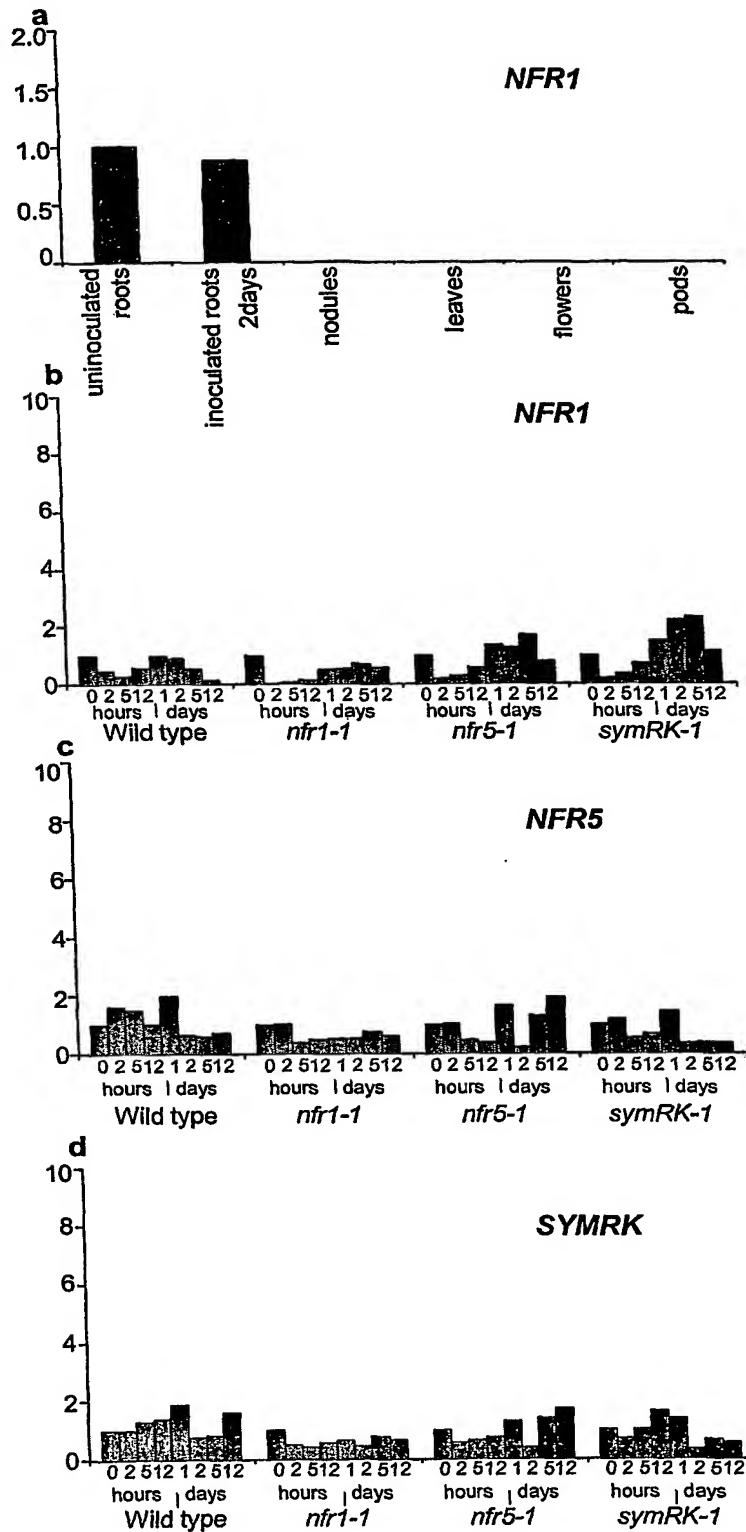


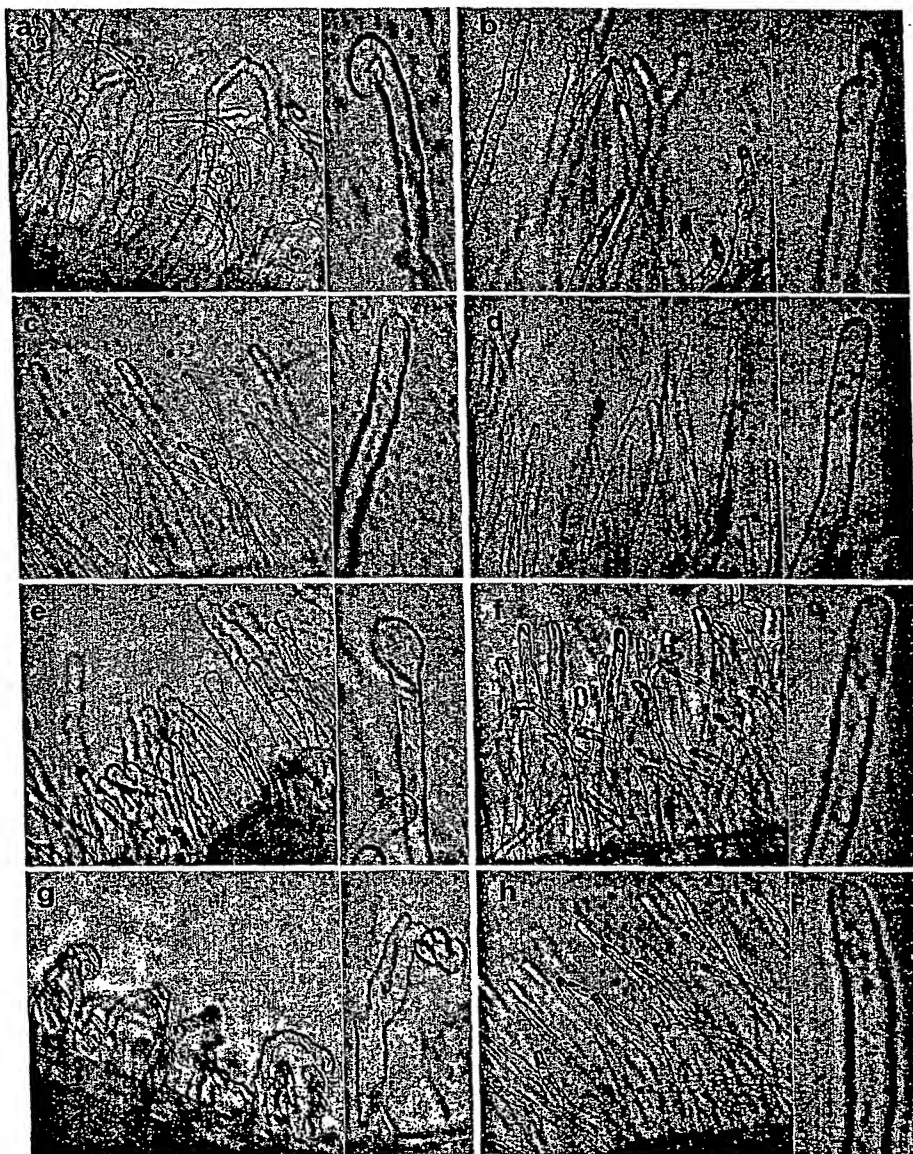
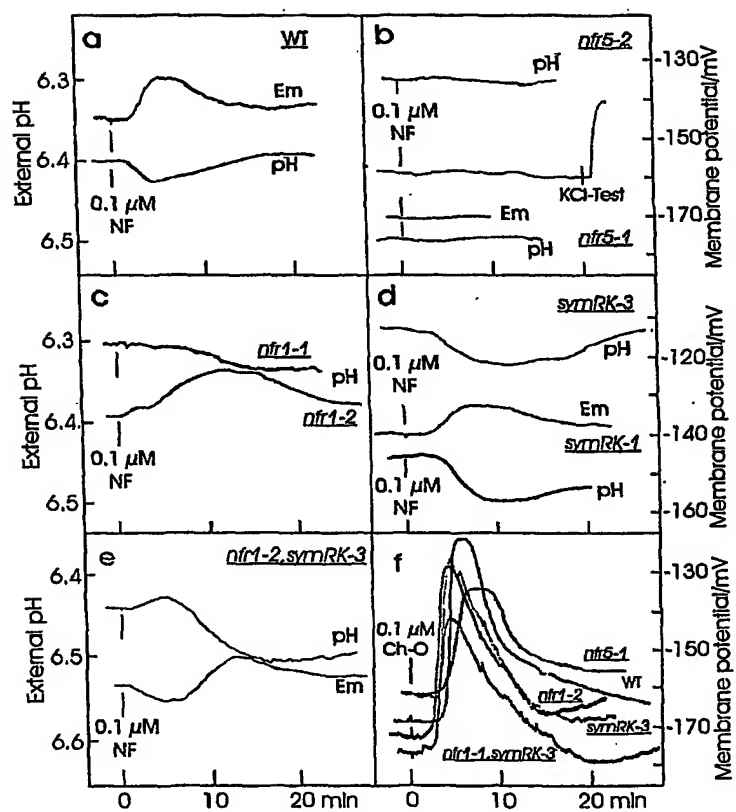
Figure 8

Figure 9



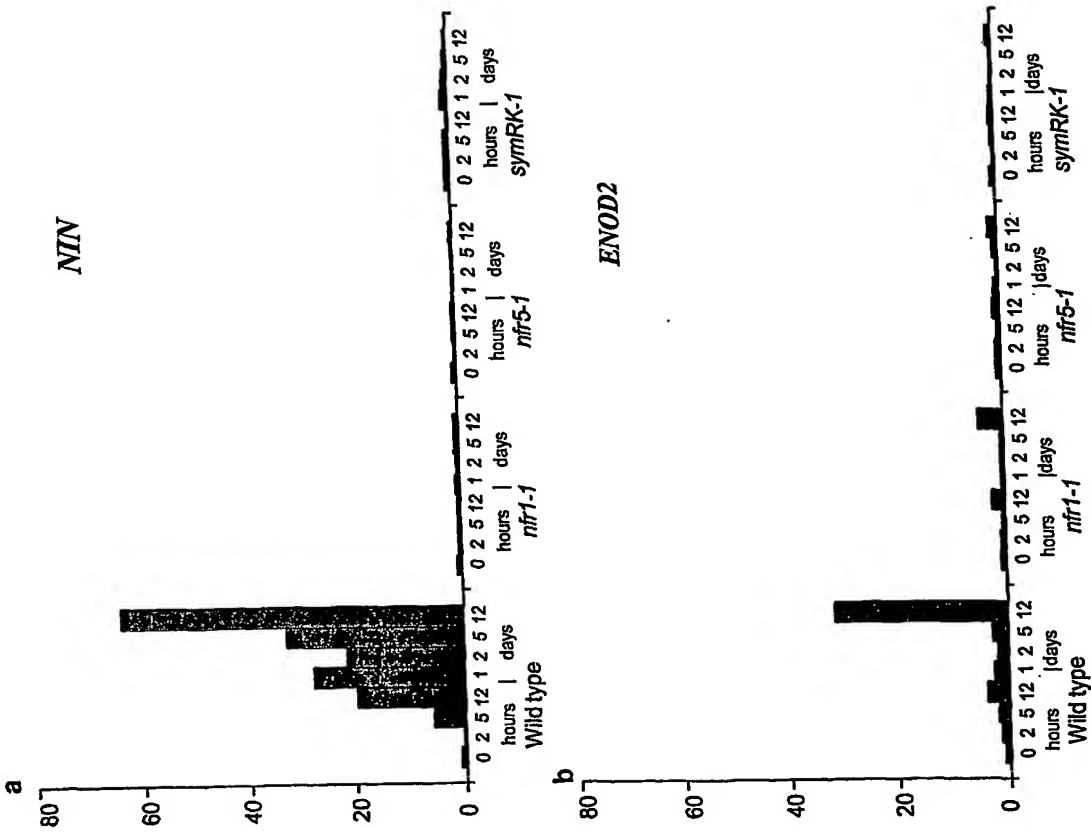


Figure 10

Figure 11

NFR1 1:MK...LKIG.LLLEFFLLGHVCFHVESNCLKG...C...D...LALASVYIL....PGVFILQNIITTFMQSEIVSSNDALTSYNKDKILNDINIQSFQRL
 NFR5 1:MAVFELTSGSLSLFLALHLLFTNIAARSEKISCPDFSCPVDSPSPSCETVYTYTAQSPENLLSFTNLSDIFDISPIARIAS...NIDAGK.DKLVPG.QVL

 NFR1 85:NIEFPQDCIGGEFLGHVFESASKGDTYETIANLYYANLITVDLLKRN SYDEKNIPVANAKVNVVNCSCGNS.QVSKDYGLFETYPITREGETLQDIAN
 NFR5 96:LVEVTQCCAGNHSSANT.SMQIQGDSYDFVATTIYENHNNWNIVQASNPVNEVILLPERVKVVFLEFCRCPKQNLKNGIQYLITYVVKPNDNVSLVSA

 NFR1 183:QSSLDAGLTQSFN.PSVNFSKDSGL.AFLPGRYKNGVYVLYHRTAGLASGAAGVIGISIACTFVILLILAFCMYVRYQKKEEKAKLPTDISMALSTQDASS
 NFR5 195:KFGASPADILTENRYGQDFTATNLPIIP...VT...QIPELTQPS..SNGRKS..SIHLLVILGITLGCITLL.TAVLTGTLVYVYCRRKALN.RTASS

 NFR1 281:SAEYETSGSGPGTASATGLTSIMVAKSMEFYSQELAKAMNNEFSLDNKICQGGFGAVYVYAEELRGKKTALIKKMDVQASTEFLOELKVTHTVHHLNVLRLIG
 NFR5 283:.AETADKLLSG.....VSGY....VSKPNVYEIDEIMEAKDESKVGES....VYKANIEGRVVAVKKIKEGGANE...ELKTILOKVNHGKLVKLMG

 NFR1 381:YC..VEGSLFLVYEHIDNGLQYDHG.SGKEP..LPWSSRVQIALDAARGLEVTHEHTVPVYIHRDVKSANILLIDKNLRCKVADFGLTKLIEVGNSTLQ
 NFR5 367:VSSGYDNCFLVYEAENGSLAEMLFKSSGTSNSLTWSORLSIAVDVAVGLQVMEHTYPRIIHRDITTSNILLIDSTFFKAKIANFAMAR.....TST..

 NFR1 476:TRLVGTFGYMEPEYAOYGDISPDKIDVYAFGVVLLFELISAKNAVIL..KTGELVAESKGLVALFEEALNKSDDPCDALRKLVDPRI GENVPEIDSVLKIAQLGR
 NFR5 459:.....NP.....MMPKIDVFAFGVLLIELLTGRKAMTTKENGCEVVMWNKMDWWEIEDIEENR...EERIRKWMDENIESEFHHIDNALSLASLAV

 NFR1 574:ACTRDNPILRPSNRSLVVALMTLSSLTEDCDDSESSYES.....QTLINLLSVR
 NFR5 540:NCTADKSLSRPSWAEIVLSLSFLTQOSSNPTLERSLTSSGLDVEDDAHIVTSITAR

